AMENDMENTS TO THE SPECIFICATION

IN THE SPECIFICATION

On page 40, line 20, please replace the original paragraph with the following amended paragraph:

-- Double-stranded cDNAs were synthesized with a SuperScriptII reverse transcriptase kit (Invitrogen) using an oligonucleotide (GACTAGTTCTAGATCGCGAGCGGCCGCCC$(T)_{15}$) (SEQ ID NO: 5) (Invitrogen) having an *Not* I site as a primer and mRNAs (Clontech) derived from human adult whole brain, human tonsil, human hippocampus, and human fetal whole brain as templates. Adaptors (Invitrogen) having *Sal* I sites were ligated to cDNAs. Subsequently, the resultants were digested with *Not* I, and then DNA fragments of 3 kb or more were purified by low melting agarose electrophoresis with 1% concentration. --

On page 48, line 4, please replace the original paragraph with the following amended paragraph:

-- Regarding the expression levels of the gene of the present invention, primer sequences that were optimal for RT-PCR were searched for using PrimerExpress 1.5 of ABI. When the sequence of the FJ04470 gene was compared with the genome sequence, the sequence matched the sequence of AC016168.18. As a result of analyzing intron and exon structures, the presence of an intron comprising approximately 2260 nucleotides were inferred in the vicinity of the nucleotide number of 2158 of FJ04470. Thus, primer positions were determined so that they

sandwiched the region. When primer 4470-2043 (5'-AGATCCATGGCACCGTGTACTAC-3') (SEQ ID NO: 6) and primer 4470-2230 (5'-GAAGATGCAACCATTGGCG-3') (SEQ ID NO: 7) are used, 188 nucleotides will be amplified in the case of cDNA and approximately 2450 nucleotides will be amplified in the case of the genome. 0.5 μl of 10 μM primer 4470-2043, 0.5 μl of 10 μM primer 4470-2230, 6.5 μl of DEPC-treated water, and 12.5 μl of SYBR Green PCR Master Mix (ABI, #4309155) were mixed to 20 μl. 1 μl of MTC Panel cDNA (Clontech) and 4 μl of DEPC-treated water (treated water) were added to the mixed solution to 25 μl. Gene amplification was carried out for 40 cycles, each cycle consisting of 50°C for 2 minutes, 95°C for 10 minutes, and 95°C for 20 seconds-60°C for 1 minute) using an ABI PRISM (registered trademark) 7700 Sequence Detection System of ABI on the MicroAmp Optical 96-Well Reaction Plate of ABI (ABI, #N801-0560). A standard curve was created using a plasmid into which a GAPDH amplicon (the expression level of the GAPDH gene was used as an internal control) had been cloned. Based on the curve, the number of copies existing in the reaction solution was calculated. Table 3 below shows the results of comparing the expression levels in different tissues using relative values obtained by dividing each expression level of the gene of the present invention by each expression level of the GAPDH gene. --